

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-3 (canceled)

4. (currently amended) The method as in or any of claims 1, 2, or 332 or 33 comprising an additional step of cleaving the at least three samples of differential isotope labeled derivatives of molecules into fragments, prior to the step of examining the at least three samples of differential isotope labeled derivatives of molecules by mass spectrometry.
5. (currently amended) The method as in or any of claims 1, 2, or 332 or 33 comprising an additional step of denaturing the molecules prior to the step of reacting the molecules with differential isotope labeled reagentsstep (ii).
6. (currently amended) The method as in or any of claims 1, 2, or 332 or 33 wherein the step of examining the at least three samples of differential isotope labeled derivatives of molecules by mass spectrometry comprises introducing the at least three samples of differential isotope labeled derivatives of molecules to a mass spectrometer using electrospray ionization.
7. (previously presented) The method of claim 6 wherein the electrospray ionization method is selected from the group consisting of nanospray, pneumatically assisted electrospray, ionspray and turboionspray.
8. (currently amended) The method as in or any of claims 1, 2, or 332 or 33 comprising an additional step of separating the at least three samples of differential isotope labeled derivatives of molecules into sub-fractions before the step of examining the at least three samples of differential isotope labeled derivatives of molecules by mass spectrometry.
9. (currently amended) The method of claim 8 wherein the step of separating the at least three samples of differential isotope labeled derivatives of molecules uses a separator selected from the group consisting of 1-D gel electrophoresis, SDS-PAGE, isoelectric focusing, 2-D gel electrophoresis, zone electrophoresis, isotachophoresis, ion exchange

chromatography, normal phase chromatography, reverse phase chromatography, hydrophobic interaction chromatography, size exclusion chromatography and any combination of these separators.

10. (currently amended) The method of claim 4 comprising an additional step of separating the fragments after the step of cleaving the at least three samples of differential isotope labeled derivatives of molecules and before the step of examining the at least three samples of differential isotope labeled derivatives of molecules.
11. (previously presented) The method of claim 10 wherein the step of separating the fragments uses a separator selected from the group consisting of liquid chromatography, high performance liquid chromatography and capillary electrophoresis.
12. (currently amended) The method as in or of claims any of claims 1, 2, or 332 or 33 comprising an additional step of analyzing the at least three samples of differential isotope labeled derivatives of molecules after the step of examining the at least three samples of differential isotope labeled derivatives of molecules by mass spectrometry.
13. (currently amended) The method of claim 12 wherein the derivatives are peptides and the step of analyzing the at least three samples of differential isotope labeled derivatives of molecules is selected from the group consisting of collision-induced dissociation in a mass spectrometer operating in MS/MS mode, peptide mass fingerprinting, peptide mapping, Edman sequencing and sequencing by sequential amino acid cleavage.
14. (currently amended) The method of claim 13, comprising an additional step of sequencing the molecules, after the step of analyzing the at least three samples of differential isotope labeled derivatives of sequencing the molecule molecules.
15. (currently amended) The method as in or of any of claims 1, 2, or 332 or 33 wherein the differential isotope labeled at least two chemically distinct reagents are an aldehyde and a reducing agent.
16. (previously presented) The method of claim 15 wherein the aldehyde is selected from the group consisting of formaldehyde and acetaldehyde.

17. (previously presented) The method of claim 15 wherein the reducing agent is selected from the group consisting of a sodium cyanoborohydride, sodium borohydride, dialkyl borane complexes and pyridine borane complexes.
18. (currently amended) The method as in or any of claims 1, 2, or 332 or 33 wherein the in any of claims 1, 2, or 3 is selected from the group consisting of cells, cellular extracts, sub-cellular extracts, cellular lysates, peptides, proteins, drugs, toxins, antibodies and pollutants.
19. (previously presented) The method of claim 18 wherein the sample comprises a protein having an amine and the protein is extracted from a cell.
20. (previously presented) The method of claim 19 wherein the amine of the protein is selected from the group consisting of a lysine residue, ornithine residue and a residue at the N-terminal amino group of the protein.
21. (currently amended) The method as in or any of claims 1, 2, or 332 or 33 wherein the step of examining the at least three samples of differential isotope labeled derivatives of molecules by mass spectrometry utilizes a mass spectrometer selected from the group consisting of:
 - (i) Fourier transform – Ion cyclotron resonance mass spectrometers (FT-ICR-MS);
 - (ii) Time of Flight mass spectrometers (TOF-MS, TOF-TOF-MS);
 - (iii) Ion trap mass spectrometers (IT);
 - (iv) Quadrupole mass spectrometers (Q-MS and QqQ-MS);
 - (v) Ion mobility mass spectrometers (IM-MS);
 - (vi) Quadrupole (or hexapole, octapole)-Time of Flight mass spectrometers (Q-TOF, and Qq-TOF); and
 - (vii) Ion trap – Time of flight mass spectrometers (IT-TOF).
22. (previously presented) The method of claim 21 comprising an additional step of combining the mass spectrometer with an ionization source.

23 (previously presented) The method of claim 22 wherein the ionization source is selected from the group consisting of electrospray ionization, matrix-assisted laser desorption and ionization (MALDI), field desorption, thermal desorption and laser desorption.

Claims 24-27 (canceled)

28. (withdrawn-currently amended) A kit comprising (i) at least three combinations of differential isotope labeled reagents, wherein each of the at least three combinations of differential isotope labeled reagents comprises at least two chemically distinct reagents, and the at least two chemically distinct reagents are present in each of the at least three combinations of differential isotope labeled reagents, and each of the at least three combinations of differential isotope labeled reagents is isotopically distinct and (ii) instructions to follow the methods of quantitative analysis of any of claims 32 or 33.

Claims 29-31 (canceled)

32. (new) A method for the simultaneous quantitative analysis of at least three samples comprising molecules, the method comprising:

- (i) providing at least three combinations of differential isotope labeled reagents, wherein each of the at least three combinations of differential isotope labeled reagents comprises at least two chemically distinct reagents, and the at least two chemically distinct reagents are present in each of the at least three combinations of differential isotope labeled reagents, and each of the at least three combinations of differential isotope labeled reagents is isotopically distinct;
- (ii) reacting (a) a first sample comprising molecules with (b) a first combination of differential isotope labeled reagents, reacting (c) a second sample comprising molecules with (d) a second combination of differential isotope labeled reagents, and reacting (e) a third sample comprising molecules with (f) a third combination of differential isotope labeled reagents, to produce at least three samples of differential isotope labeled derivatives of molecules;

- (iii) combining the at least three samples of differential isotope labeled derivatives of molecules for examination by mass spectrometry; and
- (iv) examining the at least three samples of differential isotope labeled derivatives of molecules by mass spectrometry.

33. (new) A method for the simultaneous quantitative analysis of at least three samples comprising molecules, wherein the molecules have an amine bearing an active hydrogen, the method comprising:

- (i) providing at least three combinations of differential isotope labeled reagents, wherein each of the at least three combinations of differential isotope labeled reagents comprises at least two chemically distinct reagents, and the at least two chemically distinct reagents are present in each of the at least three combinations of differential isotope labeled reagents, and each of the at least three combinations of differential isotope reagents is isotopically distinct;
- (ii) reacting (a) a first sample comprising molecules with (b) a first combination of differential isotope labeled reagents, reacting (c) a second sample comprising molecules with (d) a second combination of differential isotope labeled reagents, and reacting (e) a third sample comprising molecules with (f) a third combination of differential isotope labeled reagents, wherein the reacting results in a reductive alkylation of the amine of the molecules to alkylamine derivatives of the molecules, such that the at least three samples of differential isotope labeled derivatives of molecules are differentially isotope labeled at an alkylamine;
- (iii) combining the at least three samples of differential isotope labeled derivatives of the molecules for examination by mass spectrometry; and
- (iv) examining the at least three samples of differential isotope labeled derivatives of molecules by mass spectrometry

34. (new) A preparation for simultaneous quantitative analysis by mass spectrometry, the preparation comprising at least three samples of differential isotope labeled derivatives of

molecules, each of the at least three samples of differential isotope labeled derivatives of molecules resulting from a reaction of (a) a combination of differential isotope labeled reagents, wherein the combination of differential isotope labeled reagents comprises at least two chemically distinct reagents, and the combination of differential isotope labeled reagents is isotopically distinct with (b) a sample of molecules.

35. (new) The preparation of claim 34 wherein (a) the sample of molecules comprises molecules having an amine bearing an active hydrogen and (b) the at least three samples of differential isotope labeled derivatives of molecules comprise derivatives labeled at an alkylamine.
36. (new) A method for the quantitative analysis of at least three samples of cellular extracts, each of the at least three samples of cellular extracts comprising molecules having an amine bearing an active hydrogen, the method comprising:
 - (i) providing at least three combinations of differential isotope labeled reagents, wherein each of the at least three combinations of differential isotope labeled reagents comprises at least two chemically distinct reagents, and the at least two chemically distinct reagents are present in each of the at least three combinations of differential isotope labeled reagents, and each of the at least three combinations of differential isotope labeled reagents is isotopically distinct;
 - (ii) reacting (a) a first sample of cellular extract comprising molecules with (b) a first combination of differential isotope labeled reagents, reacting (c) a second sample of cellular extract comprising molecules with (d) a second combination of differential isotope labeled reagents, and reacting (e) a third sample of cellular extract comprising molecules with (f) a third combination of differential isotope labeled reagents, to produce at least three samples of differential isotope labeled derivatives of molecules, wherein the reacting results in a reductive alkylation of the amine of the molecules to alkylamine derivatives of the molecules, such that the at least three samples of differential labeled derivatives of molecules are differentially isotope labeled at an alkylamine;

- (iii) combining the at least three samples of differential labeled derivatives of molecules;
- (iii) separating the at least three samples of differential labeled derivatives of molecules into fractions;
- (iv) enzymatically cleaving the at least three samples of differential labeled derivatives of molecules into fragments;
- (v) separating the fragments;
- (vi) examining the fragments by mass spectrometry; and
- (vii) sequencing the fragments.